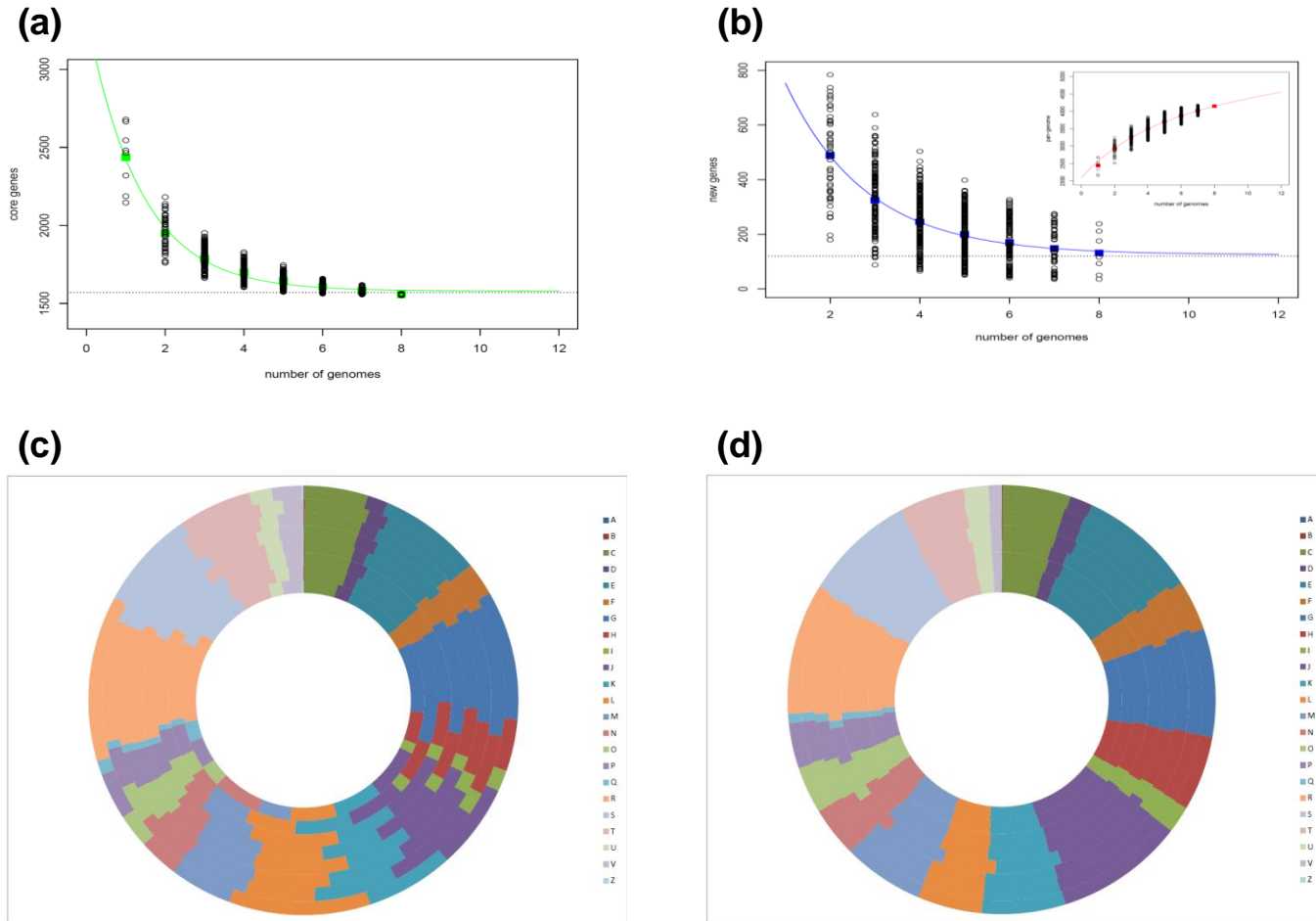
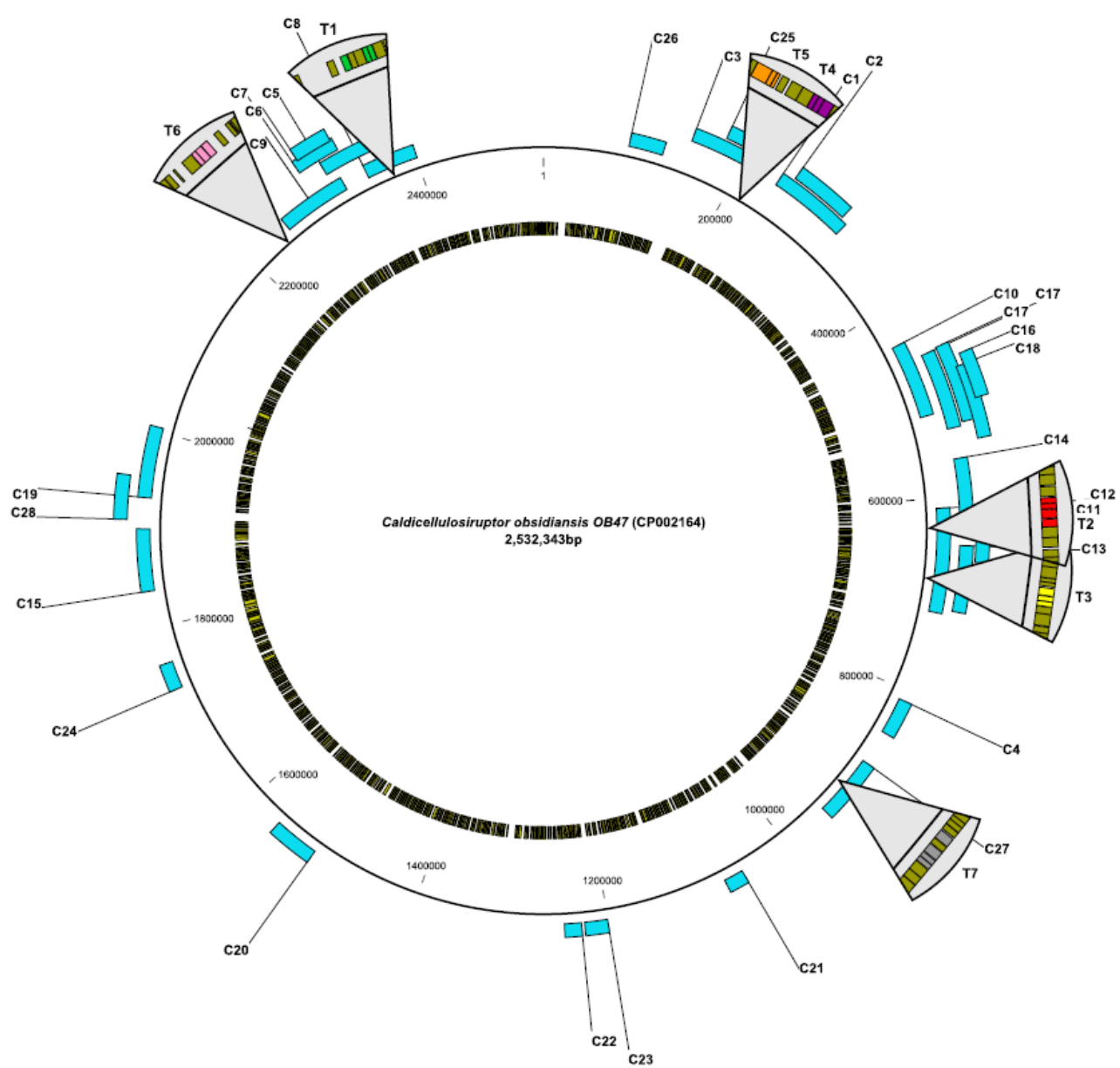


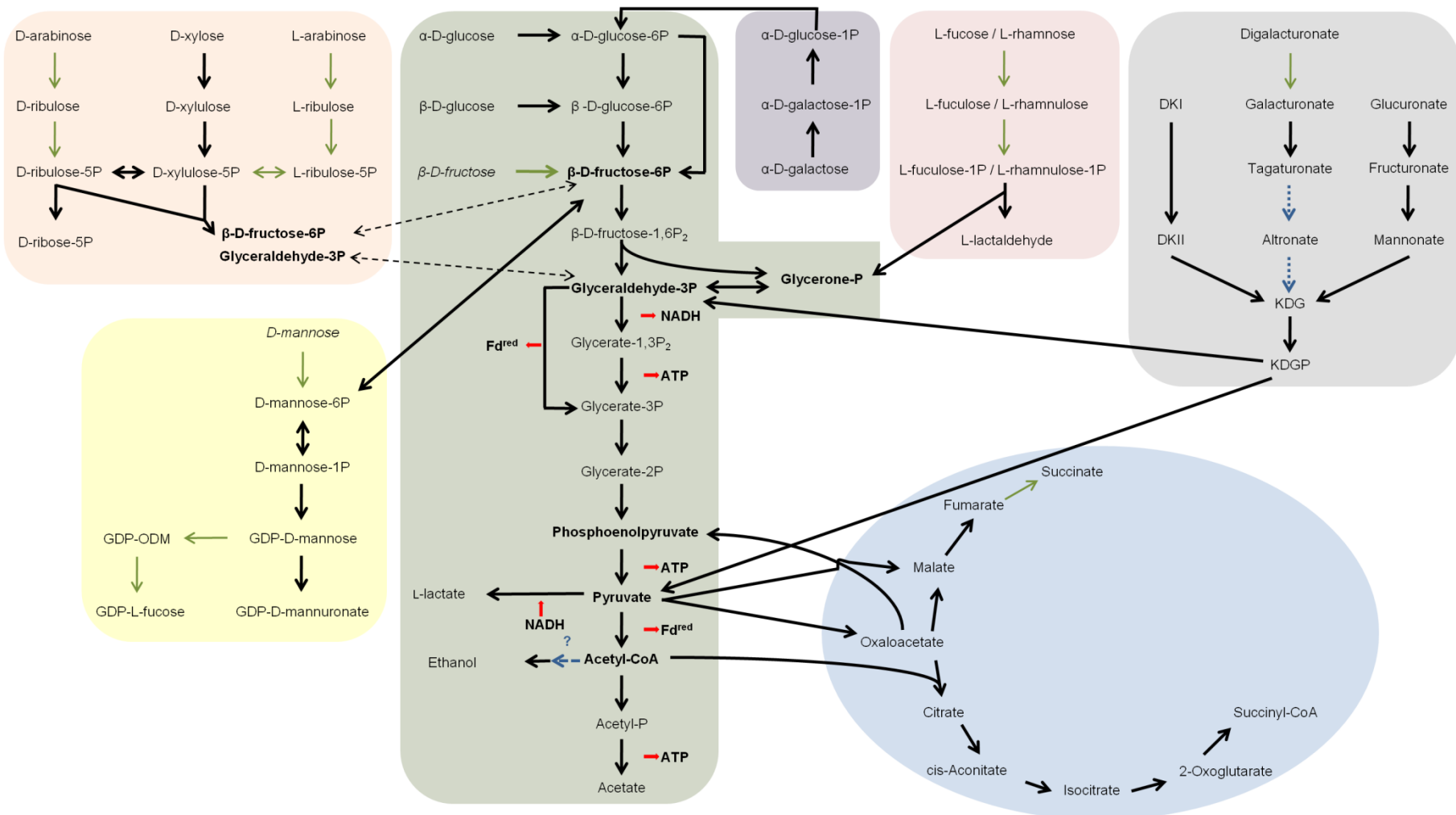
**Figure S1. Macro-synteny of geographically related species.** Alignment along the chromosomes for **(a)** the Icelandic species, *C. kristjanssonii* (top) and *C. lactoaceticus* (bottom); **(b)** the North American species, *C. obsidiensis* (top) and *C. owensensis* (bottom); and **(c)** the Russian species, *C. bescii* (top), *C. hydrothermalis* (middle) and *C. kronotskyensis* (bottom). Alignment used the Mauve Genome Alignment software package v2.0 (<http://gel.ahabs.wisc.edu/mauve/>).



**Figure S2. *Caldicellulosiruptor* pan and core genomes.** The predicted **(a)** core genome and **(b)** novel ORFs with the pan genome inset for the genus *Caldicellulosiruptor* using all eight genomes. Distribution of COG functional categories for **(c)** each individual genome and **(d)** the core genome from each of the eight sequenced *Caldicellulosiruptor* strains. For each graph, the legend indicates the COG functional category (<http://www.ncbi.nlm.nih.gov/COG/>). From outer to inner rings: *C. saccharolyticus*, *C. owensensis*, *C. obsidiansis*, *C. lactoaceticus*, *C. kronotskyensis*, *C. kristjanssonii*, *C. hydrothermalis* and *C. bescii*. Width of each bar represents the frequency (# of genes in COG/ # genes in genome) for each COG.



**Figure S3. Genomic organization of core carbohydrate transporters and carbohydrate-associated enzymes.** Numbers above ORFs and ORF clusters correspond to “Core Group” found in Supplementary Table S2. Carbohydrate-active enzymes are represented at 30x magnification for visibility. Circular wheel was drawn using the CLC Main Workbench software package (CLC Bio, [<http://www.clcbio.com>]).



**Figure S4. Carbon metabolism of *Caldicellulosiruptor* species.** Black arrows indicate that all eight sequenced species have functional homology for the particular reaction. Green arrows indicate that only some of the eight sequenced species have functional homology for the particular reaction. Double arrow dashed lines indicate where reaction products are the same. Single arrow dashed lines indicate where functional homology is unclear for a particular reaction. Intermediate products in bold font are those that connect multiple pathways. Color shading refers to metabolic pathways: blue, tricarboxylic acid pathway; grey, uronic acid metabolism; green, glycolysis; ivory, mannose metabolism; peach, non-oxidative pentose phosphate pathway and pentose interconversions; pink, deoxy sugar metabolism; purple, Leloir pathway. Abbreviations: DKII, 5-keto-4-deoxyuronate; DKII, 2,5-Diketo-3-deoxy-D-gluconate; Fd<sup>red</sup>, reduced ferredoxin; KDG, 2-Dehydro-3-deoxy-D-gluconate; KDGP, KDG phosphate; NADH, reduced nicotinamide adenine dinucleotide P, phosphate.